

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/699,652 DATE: 11/20/2000  
 TIME: 20:20:55

Input Set : A:\Pto.amc  
 Output Set: N:\CRF3\11202000\I699652.raw

2 <110> APPLICANT: Cahoon, Edgar B.  
 3 Cahoon, Rebecca E.  
 4 Kinney, Anthony J.  
 5 Rafalski, J. Antoni  
 7 <120> TITLE OF INVENTION: TRIACYLGLYCEROL LIPASES  
 9 <130> FILE REFERENCE: BB1168 US NA  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/699,652  
 C--> 12 <141> CURRENT FILING DATE: 2000-10-30  
 14 <150> PRIOR APPLICATION NUMBER: 60/083,688  
 15 <151> PRIOR FILING DATE: 1988-04-30  
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/09280  
 18 <151> PRIOR FILING DATE: 1999-04-29  
 20 <160> NUMBER OF SEQ ID NOS: 36  
 22 <170> SOFTWARE: Microsoft Office 97  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 751  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Zea mays  
 29 <400> SEQUENCE: 1  
 30 gcacgagatc accggcaaga actactgcct caacagctcc gccgtcgacg tcttctctcaa 60  
 31 gtacgagccc cagccgacct ccaccaaaac catgggtccac ttcgctcaaa ccgtgcgcga 120  
 32 cggcgtgctg accaagtacg actacgtgct gccggagcgg aacatcgcca gctacggcca 180  
 33 ggccgagccg ccggtgtacc ggaatgtccg catcccgccg agcttcccg ctttctctcag 240  
 34 ctacggcgccg cgggactcgc tcgcccagccc cgcgcgacgt cgcctctctcc tgcaggacct 300  
 35 ccggggccac gaccaggaca agctcacggt gcagtacctg gacaagtctc cgcacctctga 360  
 36 ctctcatcgc ggcgtctcgc ccaaggacta cgtctacaag gacatgacg acttctctaaa 420  
 37 ccgcttccac tagtactagc atatatatctt gcttcaatcg gtgtcgtctt cagccccagc 480  
 38 aggattagac aaaaaaagg ggggacactg cagctcgtaa acgttctcca tacagattat 540  
 39 cagagggtgaa aaccatacat gatgtaattt agcattagat agtlaaaaca tggagctgcc 600  
 40 tcagtatgga ggattgtcaa ctactctcca tcacagcagt aggtgtgatg tagaagagtg 660  
 41 attgtcacac tgtgtgtgtt gcaaatcttc aacacagtga ttactaatat aaaaaatct 720  
 42 cttgagttaa aaaaaaaaaa aaaaaaaaaa a 751  
 44 <210> SEQ ID NO: 2  
 45 <211> LENGTH: 143  
 46 <212> TYPE: PRT  
 47 <213> ORGANISM: Zea mays  
 49 <400> SEQUENCE: 2  
 50 His Glu Ile Thr Gly Lys Asn Tyr Cys Leu Asn Ser Ser Ala Val Asp  
 51 1 5 10 15  
 53 Val Phe Leu Lys Tyr Glu Pro Gln Pro Thr Ser Thr Lys Thr Met Val  
 54 20 25 30  
 56 His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr  
 57 35 40 45  
 59 Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro  
 60 50 55 60  
 62 Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser  
 63 65 70 75 80

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```

65 Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu
66                      85                      90                      95
68 Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr
69                      100                      105                      110
71 Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys
72                      115                      120                      125
74 Asp Tyr Val Tyr Lys Asp Met Ile Asp Phe Leu Asn Arg Phe Asn
75                      130                      135                      140
77 <210> SEQ ID NO: 3
78 <211> LENGTH: 647
79 <212> TYPE: DNA
80 <213> ORGANISM: Catalpa sp.
82 <400> SEQUENCE: 3
83 ttatctttca ggagagattt ttgtttgaat gctccccccg ttgagctttt tgtggaaaat 60
84 taccctcccat ctcccgtaga ttgagacccc tgtccataty gctcaaaactg tccgatatgg 120
85 gacctacccc aaatacgact acggcaatcc cagcttcaac ttggcccatg atggtagaat 180
86 cagacctccc gtttacgatt taccgaagat tccctcgac attccgctct tctaagcta 240
87 tggaggacaa gatgcattgt cggatgttaa ggatgtcgag acattgctcg atagtctcaa 300
88 gttacacgat gtggataaag tgcattgtga gtatatcaag gattatgctc atgccgactt 360
89 cattatcgga gttactgcaa aagatatagt ttataatcag attgtaactt ttttcagaaa 420
90 ccaggcttga gaggttcttg attttggagt gcttttctg tgagaatgca acagcttggt 480
91 ccactcttgt tgaatgtgaa taagccattt ccgagagatt taatggctgg taaagcttat 540
92 tagtttactc atagatacat gtaagaagca acccgataca tagtttgaat cctttatctc 600
93 gaaaagggtat tgcattctct cttctacgtc aaaaaaaaaa aaaaata 647
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 116
97 <212> TYPE: PRT
98 <213> ORGANISM: Catalpa sp.
100 <400> SEQUENCE: 4
101 Ile Glu Thr Pro Val His Met Ala Gln Thr Val Arg Tyr Gly Ile Leu
102 1                      5                      10                      15
104 Pro Lys Tyr Asp Tyr Gly Asn Pro Ser Phe Asn Leu Ala His Tyr Gly
105                      20                      25                      30
107 Glu Ser Arg Pro Pro Val Tyr Asp Leu Ser Lys Ile Pro Leu Asp Ile
108                      35                      40                      45
110 Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys
111                      50                      55                      60
113 Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys
114 65                      70                      75                      80
116 Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile
117                      85                      90                      95
119 Gly Val Thr Ala Lys Asp Ile Val Tyr Asn Glu Ile Val Thr Phe Phe
120                      100                      105                      110
122 Arg Asn Gln Ala
123                      115
125 <210> SEQ ID NO: 5
126 <211> LENGTH: 705
127 <212> TYPE: DNA
128 <213> ORGANISM: Catalpa sp.

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130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (526)
134 <220> FEATURE:
135 <221> NAME/KEY: unsure
136 <222> LOCATION: (561)
138 <220> FEATURE:
139 <221> NAME/KEY: unsure
140 <222> LOCATION: (585)
142 <220> FEATURE:
143 <221> NAME/KEY: unsure
144 <222> LOCATION: (593)
146 <220> FEATURE:
147 <221> NAME/KEY: unsure
148 <222> LOCATION: (664)
150 <220> FEATURE:
151 <221> NAME/KEY: unsure
152 <222> LOCATION: (679)
154 <400> SEQUENCE: 5
155 gcacgagcca acagcttccct aaatttagct cttctaatcc ttctctcatt atcactactc 60
156 ctacctcctc aatcattcgc ctccagccgc cgcctgtttc ttccgcagaa tgatgtcgtt 120
157 cttccgcggg acggcggtttg ctccaccgcc gtaactgtac acgggtataa atgccaagaa 180
158 tttgaagtaa cgaactgatga tggctatata ttaagcgtgc agaggattct ggagggccgg 240
159 gccggaggag gagggccgaa gcggccgcgc gttctgctgc aacatgyggt tcttgtggac 300
160 gggatqacgt ggcgtggtgaa tggaccggaa caatctttgg cgatgatatt ggcagacaat 360
161 ggggttcgaag tctggatttc taacataaga ggaactaggt ttagtcgtcg tcatgtcagc 420
162 cttgaccta ccatcctga atattggat tgggcattgg acgatctgg tgaccacga 480
W--> 163 cttaccatcc ctgacgagt tagtggtcag acaaacgggt cagaanacac actacatagg 540
W--> 164 gcaatccatg gggaaactta ntacttttgg gatcactttt agganggaaa cangttggca 600
165 gggtaaatcg gctgtatggt aagccaattg gctaacgagt catatgcaac tgctctcgag 660
W--> 166 ttgntagca gatccttgnr ggggaacaca cgatcttggc ctgag 705
168 <210> SEQ ID NO: 6
169 <211> LENGTH: 157
170 <212> TYPE: PRT
171 <213> ORGANISM: Catalpa sp.
173 <400> SEQUENCE: 6
174 Ala Arg Ala Asn Ser Phe Leu Asn Leu Ala Leu Leu Ile Leu Leu Ser
175 1 5 10 15
177 Leu Ser Leu Leu Leu Pro His Gln Ser Phe Ala Ser Ser Arg Arg Arg
178 20 25 30
180 Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser
181 35 40 45
183 Thr Ala Val Thr Val His Gly Tyr Lys Cys Gln Glu Phe Glu Val Thr
184 50 55 60
186 Thr Asp Asp Gly Tyr Ile Leu Ser Val Gln Arg Ile Leu Glu Gly Arg
187 65 70 75 80
189 Ala Gly Gly Gly Gly Pro Lys Arg Pro Pro Val Leu Leu Gln His Gly
190 85 90 95
192 Val Leu Val Asp Gly Met Thr Trp Leu Val Asn Gly Pro Glu Gln Ser

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193                    100                    105                    110  
 195 Leu Ala Met Ile Leu Ala Asp Asn Gly Phe Asp Val Trp Ile Ser Asn  
 196                    115                    120                    125  
 198 Ile Arg Gly Thr Arg Phe Ser Arg Arg His Val Ser Leu Asp Pro Thr  
 199                    130                    135                    140  
 201 Asp Pro Glu Tyr Trp Asp Trp Ala Trp Asp Asp Leu Gly  
 202 145                    150                    155

204 <210> SEQ ID NO: 7  
 205 <211> LENGTH: 859  
 206 <212> TYPE: DNA  
 207 <213> ORGANISM: Zea mays  
 209 <220> FEATURE:  
 210 <221> NAME/KEY: unsure  
 211 <222> LOCATION: (46)  
 213 <220> FEATURE:  
 214 <221> NAME/KEY: unsure  
 215 <222> LOCATION: (231)  
 217 <400> SEQUENCE: 7

W--> 218 aaagcaaaaca acggcgggaca tggcgcgccc aggaaaagcg cttgcnegcg cccagctcct 60  
 219 cctctctggtg ttcctctgac tcttagccgg tggagcccg ccatccccc ccacagacgc 120  
 220 gctacgcccgc gtctccccgc gcgcgggggc cgggtggcctc tgcacagcgc tgcctctgcc 180  
 W--> 221 gcagggttacc cgtgcaccga gcacaccggt caaacggatg atggctttct nttgtctctt 240  
 222 cagcatattc cacatggcag aaatggaatt gcagataata ctggacctcc agtttttctt 300  
 223 cagcaccggtc ttttccaggg tggagataca tggttcataa actccaatga acaatcactt 360  
 224 ggatatatcc ttgctgacaa tggttttgat gtttgggtcc qaaatggttc tggcacacyt 420  
 225 tggagtaaaag gccactctac tctctctggt catgataaag ttttctggga ttggagtttg 480  
 226 caagaccttg ctgaatacga cgttttggca atgttaagct atgtatatac agtgcacag 540  
 227 tccaaaattt tgtatgtggg acattcacag ggaactatca tgggttttgg tgcgtttaca 600  
 228 atgectgaaa cagttaaagat gataagctct gctgcgcttc tttgtcccat ttcttaacct 660  
 229 gatcacgtca gtgctagtgt tgttcttaga gcagttgcc aagcatcttg tgagatgctt 720  
 230 gttattatgg gcattccatc gttgaacttc cggagcgata tgggtgtaca gatattagat 780  
 231 tcyctgtgct atgatgaaca tttggactgc aacgatctgt tatcttcaat aacagtcaaa 840  
 232 actgttgttc aatcatctc 859

234 <210> SEQ ID NO: 8  
 235 <211> LENGTH: 286  
 236 <212> TYPE: PRT  
 237 <213> ORGANISM: Zea mays  
 239 <220> FEATURE:  
 240 <221> NAME/KEY: UNSURE  
 241 <222> LOCATION: (16)  
 243 <400> SEQUENCE: 8

W--> 244 Lys Ala Asn Asn Gly Gly His Gly Ala Pro Arg Lys Ser Ala Cys Xaa  
 245 1                    5                    10                    15  
 247 Ala Pro Ala Pro Pro Pro Arg Val Pro Leu Pro Pro Ser Arg Trp Ser  
 248                    20                    25                    30  
 250 Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg  
 251                    35                    40                    45  
 253 Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro  
 254                    50                    55                    60

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```

256 Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu
257 65 70 75 80
259 Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro
260 85 90 95
262 Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe
263 100 105 110
265 Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly
266 115 120 125
268 Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly
269 130 135 140
271 His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp
272 145 150 155 160
274 Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr
275 165 170 175
277 Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr
278 180 185 190
280 Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile
281 195 200 205
283 Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser
284 210 215 220
286 Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu
287 225 230 235 240
289 Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val
290 245 250 255
292 Gln Ile Leu Asp Ser Leu Cys Asp Asp Glu His Leu Asp Cys Asn Asp
293 260 265 270
295 Leu Leu Ser Ser Ile Thr Val Lys Thr Val Val Gln Ser Ser
296 275 280 285
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 509
300 <212> TYPE: DNA
301 <213> ORGANISM: Zea mays
303 <220> FEATURE:
304 <221> NAME/KEY: unsure
305 <222> LOCATION: (162)
307 <220> FEATURE:
308 <221> NAME/KEY: unsure
309 <222> LOCATION: (277)
311 <220> FEATURE:
312 <221> NAME/KEY: unsure
313 <222> LOCATION: (284)
315 <220> FEATURE:
316 <221> NAME/KEY: unsure
317 <222> LOCATION: (290)
319 <220> FEATURE:
320 <221> NAME/KEY: unsure
321 <222> LOCATION: (295)
323 <220> FEATURE:
324 <221> NAME/KEY: unsure

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*fyi*

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY                      DATE: 11/20/2000  
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L:11 M:270 C: Current Application Number differs, Replaced Application Number  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:163 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 L:163 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
 L:164 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 M:340 Repeated in SeqNo=5  
 L:166 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 L:218 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
 L:218 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7  
 L:221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
 M:340 Repeated in SeqNo=7  
 L:244 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
 L:244 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8  
 L:354 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
 L:354 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9  
 L:356 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
 M:340 Repeated in SeqNo=9  
 L:358 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
 L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
 L:360 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
 L:393 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
 L:393 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
 L:399 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
 M:340 Repeated in SeqNo=10  
 L:442 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 L:442 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11  
 L:445 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 M:340 Repeated in SeqNo=11  
 L:446 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
 L:486 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
 L:486 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12  
 L:489 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
 M:340 Repeated in SeqNo=12  
 L:682 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:682 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
 L:683 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 M:340 Repeated in SeqNo=15  
 L:685 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:686 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:687 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:688 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:712 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
 L:712 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
 L:721 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
 M:340 Repeated in SeqNo=16  
 L:1058 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
 L:1058 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23  
 L:1060 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23

## VERIFICATION SUMMARY

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M:340 Repeated in SeqNo=23

L:1062 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:23

L:1076 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:23

L:1077 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:23

L:1107 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:24

L:1107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24

L:1110 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:24

M:340 Repeated in SeqNo=24

L:1122 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:24

L:1175 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:25

L:1175 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25

L:1208 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:26

L:1208 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26

L:1299 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:27

L:1299 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27

L:1300 M:258 W: Mandatory Feature missing, &lt;223&gt; not found for SEQ ID#:27

M:340 Repeated in SeqNo=27